

Serial Number: 09/738,672CRF Processing Date: 3-20-2002Edited by: M. SPENCER

Verified by: \_\_\_\_\_ (STIC staff)

- ☐ Changed a file from non-ASCII to ASCII
- ☐ Changed the margins in cases where the sequence text was "wrapped" down to the next line.
- ☐ Edited a format error in the Current Application Data section, specifically: \_\_\_\_\_
- ☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other \_\_\_\_\_
- ☐ Added the mandatory heading and subheadings for "Current Application Data". **ENTERED**
- ☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.
- ☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically: \_\_\_\_\_
- ☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were: \_\_\_\_\_
- ☐ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited: \_\_\_\_\_
- ☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.
- ☐ Inserted colons after headings/subheadings. Headings edited included: \_\_\_\_\_
- ☐ Deleted extra, invalid, headings used by an applicant, specifically: \_\_\_\_\_
- ☐ Deleted: ☐ non-ASCII "garbage" at the beginning/end of files; ☐ secretary initials/filename at end of file; ☐ page numbers throughout text; ☐ other invalid text, such as \_\_\_\_\_
- ☐ Inserted mandatory headings, specifically: \_\_\_\_\_
- ☐ Corrected an obvious error in the response, specifically: \_\_\_\_\_
- ☐ Edited identifiers where upper case is used but lower case is required, or vice versa.
- ☒ Corrected an error in the Number of Sequences field, specifically:  
SEQ ID # 2, 4, 6
- ☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.
- ☐ Deleted *ending* stop codon in amino acid sequences and adjusted the "(A)Length:" field accordingly (error due to a PatentIn bug). Sequences corrected: \_\_\_\_\_
- ☐ Other: \_\_\_\_\_

\*Examiner: The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.

3/1/95

# 7



OIEP

## RAW SEQUENCE LISTING

DATE: 03/20/2002

PATENT APPLICATION: US/09/734,672

TIME: 12:15:01

Input Set : A:\pto\_ms.txt

Output Set: N:\CRF3\03202002\I734672.raw

**ENTERED**

## SEQUENCE LISTING

## 3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Murphy, Patricia D.

6 Allen, Antonette C.

7 Alvares, Christopher P.

8 Critz, Brenda S.

9 Olson, Sheri J.

10 Schelter, Denise B.

11 Zeng, Bin

14 (ii) TITLE OF INVENTION: Coding Sequences of the Human

15 BRCA1 Gene

17 (iii) NUMBER OF SEQUENCES: 72

19 (iv) CORRESPONDENCE ADDRESS:

20 (A) ADDRESSEE: Morgan Lewis &amp; Bockius LLP

21 (B) STREET: 1111 Pennsylvania Ave., N.W.

22 (C) CITY: Washington

23 (D) STATE: District of Columbia

24 (E) COUNTRY: USA

25 (F) ZIP: 20004

27 (v) COMPUTER READABLE FORM:

28 (A) MEDIUM TYPE: Floppy disk

29 (B) COMPUTER: IBM PC compatible

30 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

31 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

33 (vi) CURRENT APPLICATION DATA:

C--&gt; 34 (A) APPLICATION NUMBER: US/09/734,672

C--&gt; 35 (B) FILING DATE: 03-Dec-2000

37 (vii) PRIOR APPLICATION DATA:

38 (A) APPLICATION NUMBER: US 08/966,436

39 (B) FILING DATE: 07-Nov-97

41 (A) APPLICATION NUMBER: US 08/598,591

42 (B) FILING DATE: 12-Feb-96

44 (viii) ATTORNEY/AGENT INFORMATION:

45 (A) NAME: Michael S. Tuscan

46 (B) REGISTRATION NUMBER: 43,210

47 (C) REFERENCE/DOCKET NUMBER: 44921-5055-02-US

49 (ix) TELECOMMUNICATION INFORMATION:

50 (A) TELEPHONE: 202-739-3000

51 (B) TELEFAX: 202-739-3001

55 (2) INFORMATION FOR SEQ ID NO: 1:

57 (i) SEQUENCE CHARACTERISTICS:

58 (A) LENGTH: 5711 base pairs

59 (B) TYPE: nucleic acid

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60      (C) STRANDEDNESS: Not Relevant
61      (D) TOPOLOGY: linear
63      (ii) MOLECULE TYPE: cDNA
65      (vi) ORIGINAL SOURCE:
66          (A) ORGANISM: Homo sapiens
67          (B) STRAIN: BRCA1
69      (viii) POSITION IN GENOME:
70          (A) CHROMOSOME/SEGMENT: 17
71          (B) MAP POSITION: 17q21
76      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
78 AGCTCGCTGA GACTTCCTGG ACCCCGCACC AGGCTGTGGG GTTTCCTCAGA TAACTGGGCC      60
80 CCTGCGCTCA GGAGGCCTTC ACCCTCTGCT CTGGGTAAAG TTCATTGGAA CAGAAAAGAAA      120
82 TGGATTTATC TGCTCTTCGC GTTGAAGAAG TACAAAATGT CATTAATGCT ATGCAGAAAA      180
84 TCTTAGAGTG TCCCATCTGT CTGGAGTTGA TCAAGGAACC TGTCTCCACA AAGTGTGACC      240
86 ACATATTTTG CAAATTTTGC ATGCTGAAAC TTCTCAACCA GAAGAAAGGG CCTTCACAGT      300
88 GTCCTTTATG TAAGAAATGAT ATAACCAAAA GGAGCTACA AGAAAGTACG AGATTAGTC      360
90 AACTTGTGTA AGAGCTATTG AAAATCATTG GTGCTTTTCA GCTTGACACA GGTTTGGAGT      420
92 ATGCAAACAG CTATAATTTT GCAAAAAAGG AAAATAACTC TCCTGAACAT CTAAAAGATG      480
94 AAGTTTCTAT CATCCAAAGT ATGGGCTACA GAAACCGTGC CAAAAGACTT CTACAGAGTG      540
96 AACCCGAAAA TCCTTCCTTG CAGGAAACCA GTCTCAGTGT CCAACTCTCT AACCTTGGAA      600
98 CTGTGAGAAC TCTGAGGACA AAGCAGCGGA TACAACCTCA AAAGACGTCT GTCTACATTG      660
100 AATTGGGATC TGATTCTTCT GAAGATACCG TTAATAAGGC AACTTATTGC AGTGTGGGAG      720
102 ATCAAGAATT GTTACAAATC ACCCTCAAG GAACCAGGGA TGAAATCAGT TTGGATTCTG      780
104 CAAAAAAGGC TGCTTGTAAC TTTTCTGAGA CGGATGTAAC AAATACTGAA CATCATCAAC      840
106 CCAGTAATAA TGATTGAAC ACCACTGAGA AGCGTGCAGC TGAGAGGCAT CCAGAAAAGT      900
108 ATCAGGGTAG TTCTGTTTCA AACTTGCATG TGGAGCCATG TGGCACAAT ACTCATGCCA      960
110 GCTCATTACA GCATGAGAAC AGCAGTTTAT TACTCACTAA AGACAGAATG AATGTAGAAA      1020
112 AGGCTGAATT CTGTAATAAA AGCAAAACAGC CTGGCTTAGC AAGGAGCCAA CATAACAGAT      1080
114 GGGCTGGAAG TAAGGAAACA TGTAATGATA GGCGGACTCC CAGCACAGAA AAAAAGGTAG      1140
116 ATCTGAATGC TGATCCCCTG TGTGAGAGAA AAGAATGGAA TAAGCAGAAA CTGCCATGCT      1200
118 CAGAGAATCC TAGAGATACT GAAGATGTTT CTTGGATAAC ACTAAATAGC AGCATTGAGA      1260
120 AAGTTAATGA GTGGTTTTCC AGAAGTGATG AACTGTTAGG TTCTGATGAC TCACATGATG      1320
122 GGGAGTCTGA ATCAAATGCC AAAGTAGCTG ATGTATTGGA CGTTCTAAAT GAGGTAGATG      1380
124 AATATTCTGG TTCTTCAGAG AAAATAGACT TACTGGCCAG TGATCCTCAT GAGGCTTTAA      1440
126 TATGTAAAAG TGAAAGAGTT CACTCCAAAT CAGTAGAGAG TAATATTGAA GACAAAATAT      1500
128 TTGGGAAAAC CTATCGGAAG AAGGCAAGCC TCCCCAACTT AAGCCATGTA ACTGAAAATC      1560
130 TAATTATAGG AGCATTTGTT ACTGAGCCAC AGATAATACA AGAGCGTCCC CTCACAAATA      1620
132 AATTAAAGCG TAAAAGGAGA CCTACATCAG GCCTTCATCC TGAGGATTTT ATCAAGAAAG      1680
134 CAGATTTGGC AGTTCAAAAAG ACTCCTGAAA TGATAAATCA GGGAACTAAC CAAACGGAGC      1740
136 AGAATGGTCA AGTGATGAAT ATTACTAATA GTGGTCATGA GAATAAAACA AAAGGTGATT      1800
138 CTATTGAGAA TGAGAAAAAT CCTAACCCAA TAGAATCACT CGAAAAAGAA TCTGCTTTCA      1860
140 AAACGAAAGC TGAACCTATA AGCAGCAGTA TAAGCAATAT GGAATCGAA TTAAATATCC      1920
142 ACAATTCAAA AGCACCTAAA AAGAATAGGC TGAGGAGGAA GTCTTCTACC AGGCATATTC      1980
144 ATGCGCTTGA ACTAGTAGTC AGTAGAATC TAAGCCCACC TAATTGTACT GAATTGCAAA      2040
146 TTGATAGTTG TTCTAGCAGT GAAGAGATAA AGAAAAAACA GTACAACCAA ATGCCAGTCA      2100
148 GGCACAGCAG AAACCTACAA CTCATGGAAG GTAAAGAACCC TGCAACTGGA GCCAAGAAGA      2160
150 GTAACAAGCC AAATGAACAG ACAAGTAAAA GACATGACAG TGATACTTTC CCAGAGCTGA      2220
152 AGTTAACAAA TGCACCTGGT TCTTTTACTA AGTGTTCAAA TACCAGTGAA CTTAAAGAAT      2280
154 TTGTCAATCC TAGCCTTCCA AGAGAAGAAA AAGAAGAGAA ACTAGAAACA GTTAAAGTGT      2340

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156	CTAATAATGC	TGAAGACCCC	AAAGATCTCA	TGTTAAGTGG	AGAAAGGGTT	TTGCAAACCTG	2400
158	AAAGATCTGT	AGAGAGTAGC	AGTATTTTCA	TGGTACCTGG	TACTGATTAT	GGCACTCAGG	2460
160	AAAGTATCTC	GTTACTGGAA	GTTAGCACTC	TAGGGAAGGC	AAAAACAGAA	CCAAATAAAT	2520
162	GTGTGAGTCA	GTGTGCAGCA	TTTGA AAAACC	CCAAGGGACT	AATTCATGGT	TGTTCCAAAG	2580
164	ATAATAGAAA	TGACACAGAA	GGCTTTAAGT	ATCCATTGGG	ACATGAAGTT	AACCACAGTC	2640
166	GGGAAACAAG	CATAGAAAATG	GAAGAAAAGT	AACTTGATGC	TCAGTATTTG	CAGAATACAT	2700
168	TCAAGGTTTC	AAAGCGCCAG	TCATTTGCTC	TGTTTTCAAA	TCCAGGAAAT	GCAGAAGAGG	2760
170	AATGTGCAAC	ATTCTCTGCC	CACTCTGGGT	CCTTAAAGAA	ACAAAGTCCA	AAAGTCACTT	2820
172	TTGAATGTGA	ACAAAAGGAA	GAAAAATCAAG	GAAAGAATGA	GTCTAATATC	AAGCCTGTAC	2880
174	AGACAGTTAA	TATCACTGCA	GGCTTTCCCTG	TGGTTGGTCA	GAAAGATAAG	CCAGTTGATA	2940
176	ATGCCAAATG	TAGTATCAAA	GGAGGCTCTA	GGTTTTGTCT	ATCATCTCAG	TTCAGAGGCA	3000
178	ACGAAACTGG	ACTCATTACT	CCAAATAAAC	ATGGACTTTT	ACAAAAACCA	TATCGTATAC	3060
180	CACCACTTTT	TCCCATCAAG	TCATTTGTGA	AAACTAAATG	TAAGAAAAAT	CTGCTAGAGG	3120
182	AAAACTTTGA	GGAACATTCA	ATGTCACCTG	AAAGAGAAAT	GGGAAATGAG	AACATTCCAA	3180
184	GTACAGTGAG	CACAATTAGC	CGTAATAACA	TTAGAGAAAA	TGTTTTTAAA	GGAGCCAGCT	3240
186	CAAGCAATAT	TAATGAAGTA	GGTTCAGTA	CTAATGAAGT	GGGCTCCAGT	ATTAATGAAA	3300
188	TAGGTTCCAG	TGATGAAAAC	ATTCAAGCAG	AACTAGGTAG	AAACAGAGGG	CCAAAATTGA	3360
190	ATGCTATGCT	TAGATTAGGG	GTTTTGCAAC	CTGAGGTCTA	TAAACAAAGT	CTTCCTGGAA	3420
192	GTAATTGTAA	GCATCCTGAA	ATAAAAAAGC	AAGAATATGA	AGAAGTAGTT	CAGACTGTTA	3480
194	ATACAGATTT	CTCTCCATAT	CTGATTTTCA	ATAACTTAGA	ACAGCCTATG	GGAAGTAGTC	3540
196	ATGCATCTCA	GGTTTGTTCT	GAGACACCTG	ATGACCTGTT	AGATGATGGT	GAAATAAAGG	3600
198	AAGATACTAG	TTTTTGCTGAA	AATGACATTA	AGGAAAGTTC	TGCTGTTTTT	AGCAAAAAGC	3660
200	TCCAGAGAGG	AGAGCTTAGC	AGGAGTCCTA	GCCCTTTCAC	CCATACACAT	TTGGCTCAGG	3720
202	GTTACCGAAG	AGGGGCCAAG	AAATTAGAGT	CCTCAGAAGA	GAACCTATCT	AGTGAGGATG	3780
204	AAGAGCTTCC	CTGCTTCCAA	CACTTGTTAT	TTGGTAAAGT	AAACAATATA	CCTTCTCAGT	3840
206	CTACTAGGCA	TAGCACCGTT	GCTACCGAGT	GTCTGTCTAA	GAACACAGAG	GAGAATTTAT	3900
208	TATCATTTGAA	GAATAGCTTA	AATGACTGCA	GTAACAGGTT	AATATTGGCA	AAGGCATCTC	3960
210	AGGAACATCA	CCTTAGTGAG	GAAAACAAAAT	GTTCTGCTAG	CTTGTTTTCT	TCACAGTGCA	4020
212	GTGAATTGGA	AGACTTGACT	GCAAATACAA	ACACCCAGGA	TCCTTTCTTG	ATTGGTTCTT	4080
214	CCAAACAAAT	GAGGCATCAG	TCTGAAAGCC	AGGGAGTTGG	TCTGAGTGAC	AAGGAATTGG	4140
216	TTTCAGATGA	TGAAGAAAGA	GGAACGGGCT	TGGAAGAAAA	TAATCAAGAA	GAGCAAAGCA	4200
218	TGGATTCAAA	CTTAGGTGAA	GCAGCATCTG	GGTGTGAGAG	TGAAACAAGC	GTCTCTGAAG	4260
220	ACTGCTCAGG	GCTATCCTCT	CAGAGTGACA	TTTTAACCAC	TCAGCAGAGG	GATACCATGC	4320
222	AACATAACCT	GATAAAGCTC	CAGCAGGAAA	TGGCTGAACT	AGAAGCTGTG	TTAGAACAGC	4380
224	ATGGGAGCCA	GCCTTCTAAC	AGCTACCCTT	CCATCATAAG	TGACTCCTCT	GCCCTTGAGG	4440
226	ACCTGCGAAA	TCCAGAACAA	AGCACATCAG	AAAAAGCAGT	ATTAACCTCA	CAGAAAAGTA	4500
228	GTGAATACCC	TATAAGCCAG	AATCCAGAAG	GCCTTTCTGC	TGACAAGTTT	GAGGTGTCTG	4560
230	CAGATAGTTC	TACCAGTAAA	AATAAAGAAC	CAGGAGTGGA	AAGGTCATCC	CCTTCTAAAT	4620
232	GCCCATCATT	AGATGATAGG	TGGTACATGC	ACAGTTGCTC	TGGGAGTCTT	CAGAAATAGAA	4680
234	ACTACCCATC	TCAAGAGGAG	CTCATTAAGG	TTGTTGATGT	GGAGGAGCAA	CAGCTGGAAG	4740
236	AGTCTGGGCC	ACACGATTTG	ACGGAAACAT	CTTACTTGCC	AAGGCAAGAT	CTAGAGGGAA	4800
238	CCCCTTACCT	GGAATCTGGA	ATCAGCCTCT	TCTCTGATGA	CCCTGAATCT	GATCCTTCTG	4860
240	AAGACAGAGC	CCCAGAGTCA	GCTCGTGTG	GCAACATACC	ATCTTCAACC	TCTGCATTGA	4920
242	AAGTTCCCCA	ATTGAAAGTT	GCAGAATCTG	CCCAGGGTCC	AGCTGCTGCT	CATACTACTG	4980
244	ATACTGCTGG	GATAATGCA	ATGGAAGAAA	GTGTGAGCAG	GGAGAAGCCA	GAATTGACAG	5040
246	CTTCAACAGA	AAGGGTCAAC	AAAAGAATGT	CCATGGTGGT	GTCTGGCCTG	ACCCAGAAAG	5100
248	AATTTATGCT	CGTGTACAAG	TTTGCCAGAA	AACACCACAT	CACTTTAACT	AATCTAATTA	5160
250	CTGAAGAGAC	TACTCATGTT	GTTATGAAAA	CAGATGCTGA	GTTTGTGTGT	GAACGGACAC	5220
252	TGAAATATTT	TCTAGGAATT	GCGGGAGGAA	AATGGGTAGT	TAGCTATTTT	TGGGTGACCC	5280

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DATE: 03/20/2002

PATENT APPLICATION: US/09/734,672

TIME: 12:15:01

Input Set : A:\pto\_ms.txt

Output Set: N:\CRF3\03202002\I734672.raw

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254 AGTCTATTAA AGAAAGAAAA ATGCTGAATG AGCATGATTT TGAAGTCAGA GGAGATGTGG 5340
256 TCAATGGAAG AAACCACCAA GGTCCAAAGC GAGCAAGAGA ATCCCAGGAC AGAAAGATCT 5400
258 TCAGGGGGCT AGAAATCTGT TGCTATGGGC CCTTCACCAA CATGCCCACA GATCAACTGG 5460
260 AATGGATGGT ACAGCTGTGT GGTGCTTCTG TGGTGAAGGA GCTTTCATCA TTCACCCTTG 5520
262 GCACAGGTGT CCACCCAATT GTGGTTGTGC AGCCAGATGC CTGGACAGAG GACAATGGCT 5580
264 TCCATGCAAT TGGGCAGATG TGTGAGGCAC CTGTGGTGAC CCGAGAGTGG GTGTTGGACA 5640
266 GTGTAGCACT CTACCAGTGC CAGGAGCTGG ACACCTACCT GATACCCCAG ATCCCCCACA 5700
268 GCCACTACTG A 5711

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(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1863 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: Not Relevant

W--&gt; (D) TOPOLOGY: Not Relevant

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(B) STRAIN: BRCA1

(viii) POSITION IN GENOME:

(A) CHROMOSOME/SEGMENT: 17

(B) MAP POSITION: 17q21

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

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292 Met Asp Leu Ser Ala Leu Arg Val Glu Glu Val Gln Asn Val Ile Asn
293 1 5 10 15
295 Ala Met Gln Lys Ile Leu Glu Cys Pro Ile Cys Leu Glu Leu Ile Lys
296 20 25 30
298 Glu Pro Val Ser Thr Lys Cys Asp His Ile Phe Cys Lys Phe Cys Met
299 35 40 45
301 Leu Lys Leu Leu Asn Gln Lys Lys Gly Pro Ser Gln Cys Pro Leu Cys
302 50 55 60
304 Lys Asn Asp Ile Thr Lys Arg Ser Leu Gln Glu Ser Thr Arg Phe Ser
305 65 70 75 80
307 Gln Leu Val Glu Glu Leu Leu Lys Ile Ile Cys Ala Phe Gln Leu Asp
308 85 90 95
310 Thr Gly Leu Glu Tyr Ala Asn Ser Tyr Asn Phe Ala Lys Lys Glu Asn
311 100 105 110
313 Asn Ser Pro Glu His Leu Lys Asp Glu Val Ser Ile Ile Gln Ser Met
314 115 120 125
316 Gly Tyr Arg Asn Arg Ala Lys Arg Leu Leu Gln Ser Glu Pro Glu Asn
317 130 135 140
319 Pro Ser Leu Gln Glu Thr Ser Leu Ser Val Gln Leu Ser Asn Leu Gly
320 145 150 155 160
322 Thr Val Arg Thr Leu Arg Thr Lys Gln Arg Ile Gln Pro Gln Lys Thr
323 165 170 175
325 Ser Val Tyr Ile Glu Leu Gly Ser Asp Ser Ser Glu Asp Thr Val Asn
326 180 185 190
328 Lys Ala Thr Tyr Cys Ser Val Gly Asp Gln Glu Leu Leu Gln Ile Thr
329 195 200 205
331 Pro Gln Gly Thr Arg Asp Glu Ile Ser Leu Asp Ser Ala Lys Lys Ala

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Input Set : A:\pto\_ms.txt

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332	210	215	220
334	Ala Cys Glu Phe Ser Glu Thr Asp Val Thr Asn Thr Glu His His Gln		
335	225	230	235
337	Pro Ser Asn Asn Asp Leu Asn Thr Thr Glu Lys Arg Ala Ala Glu Arg		
338		245	250
340	His Pro Glu Lys Tyr Gln Gly Ser Ser Val Ser Asn Leu His Val Glu		
341		260	265
343	Pro Cys Gly Thr Asn Thr His Ala Ser Ser Leu Gln His Glu Asn Ser		
344		275	280
346	Ser Leu Leu Leu Thr Lys Asp Arg Met Asn Val Glu Lys Ala Glu Phe		
347		290	295
349	Cys Asn Lys Ser Lys Gln Pro Gly Leu Ala Arg Ser Gln His Asn Arg		
350	305	310	315
352	Trp Ala Gly Ser Lys Glu Thr Cys Asn Asp Arg Arg Thr Pro Ser Thr		
353		325	330
355	Glu Lys Lys Val Asp Leu Asn Ala Asp Pro Leu Cys Glu Arg Lys Glu		
356		340	345
358	Trp Asn Lys Gln Lys Leu Pro Cys Ser Glu Asn Pro Arg Asp Thr Glu		
359		355	360
361	Asp Val Pro Trp Ile Thr Leu Asn Ser Ser Ile Gln Lys Val Asn Glu		
362		370	375
364	Trp Phe Ser Arg Ser Asp Glu Leu Leu Gly Ser Asp Asp Ser His Asp		
365		385	390
367	Gly Glu Ser Glu Ser Asn Ala Lys Val Ala Asp Val Leu Asp Val Leu		
368		405	410
370	Asn Glu Val Asp Glu Tyr Ser Gly Ser Ser Glu Lys Ile Asp Leu Leu		
371		420	425
373	Ala Ser Asp Pro His Glu Ala Leu Ile Cys Lys Ser Glu Arg Val His		
374		435	440
376	Ser Lys Ser Val Glu Ser Asn Ile Glu Asp Lys Ile Phe Gly Lys Thr		
377		450	455
379	Tyr Arg Lys Lys Ala Ser Leu Pro Asn Leu Ser His Val Thr Glu Asn		
380		465	470
382	Leu Ile Ile Gly Ala Phe Val Thr Glu Pro Gln Ile Ile Gln Glu Arg		
383		485	490
385	Pro Leu Thr Asn Lys Leu Lys Arg Lys Arg Arg Pro Thr Ser Gly Leu		
386		500	505
388	His Pro Glu Asp Phe Ile Lys Lys Ala Asp Leu Ala Val Gln Lys Thr		
389		515	520
391	Pro Glu Met Ile Asn Gln Gly Thr Asn Gln Thr Glu Gln Asn Gly Gln		
392		530	535
394	Val Met Asn Ile Thr Asn Ser Gly His Glu Asn Lys Thr Lys Gly Asp		
395		545	550
397	Ser Ile Gln Asn Glu Lys Asn Pro Asn Pro Ile Glu Ser Leu Glu Lys		
398		565	570
400	Glu Ser Ala Phe Lys Thr Lys Ala Glu Pro Ile Ser Ser Ser Ile Ser		
401		580	585
402	Asn Met Glu Leu Glu Leu Asn Ile His Asn Ser Lys Ala Pro Lys Lys		
403		595	600

## VERIFICATION SUMMARY

DATE: 03/20/2002

PATENT APPLICATION: US/09/734,672

TIME: 12:15:02

Input Set : A:\pto\_ms.txt

Output Set: N:\CRF3\03202002\I734672.raw

L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]  
L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]  
L:276 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=2  
L:861 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=4  
L:1446 M:246 W: Invalid value of Alpha Sequence Header Field, [TOPOLOGY:], SeqNo=6